Amendments to the Specification:

Please amend the figure description beginning on page 3, line 19 as follows:

Figure 2 is the DNA sequence, SEQ ID NO. 3, of the promoter of the murine $\alpha_{1B}$ adrenergic receptor.

Please amend the figure description beginning on line 22 of page 3, as follows:

Figure 4. (A) A map of the transgene construct showing the size of EcoRI fragments and the binding sites for $\alpha_{1B}$ - and SV40-specific southern probes. Three different transgenes were constructed with the only difference between each being the $\alpha_{1B}$AR cDNA used (either the wild-type (WT), single mutant or triple mutant cDNA). Transgenic animals whose genome contain the wild-type transgene are designated W; transgenic animals whose genome contain the single mutant transgene are designated S; and transgenic animals whose genome contain the triple mutant transgene are designated T. Each founder transgenic animal and its progeny are also given a numerical designation. For example, one of the founder transgenic animals whose genome contains the wild-type transgene, and its progeny, is referred to as "W1", while another transgenic founder animal whose genome contains the wild-type transgene, and its progeny, is referred to as "W2". (B) Southern blot analysis of genomic DNA from nontransgenic (NT)(-/-), heterozygous (+/-) and homozygous (+/+) W2 mice. Tail DNA samples were digested with EcoRI, run on 0.8% agarose gels, transferred to nitrocellulose and probed with either the $\alpha_{1B}$ probe or the SV40 probe. The $\alpha_{1B}$ probe hybridized to 3.0 and 1.6 kb fragments which represented the endogenous $\alpha_{1B}$AR gene and the transgene respectively. Comparatively, the SV40 probe hybridized only to a 1.4 kb fragment which represented the transgene. (**C**) $B_{max}$ determination was carried out via saturation binding in various $\alpha_{1B}$AR -positive and -negative tissues using the $\alpha_1$-antagonist 2-[$\beta$-(4-hydroxyl-3-[$^{125}$I]iodophenyl)ethylaminomethyl]tetralone ([$^{125}$I]HEAT) as the radioligand. $B_{max}$ values in W2+/- mice that were significantly different from the corresponding non-transgenic (NT) values are labeled with an asterisk. Error bars represent SEM (N>5 for each tissue) and significance was determined using analysis of variance with a two-tailed Student's t test ($p<0.05$). (D) Inositol tri-phosphate ($IP_3$)levels. Error bars represent SEM (n=3 for each line) and significance was determined using analysis of variance with a two-tailed Student's *t* test ($p<0.05$). The asterisk (*) indicates significance from the NT

group. The dagger (†) indicates significant increases compared to the W2+/- group. The double cross (‡) indicates significant increases compared to the S 1+/- group.. (**E**) Hybridization pattern of the SV40 probe in a section cut from a NT mouse. (**F**) Hybridization pattern of the $\alpha_{1B}$ probe to endogenously expressed $\alpha_{1B}$AR transcripts in a NT brain section. (**G**) Hybridization of the SV40 probe to message transcribed from the transgene in the brain of a W2+/- mouse. Cx = cortex; Rt = reticular thalamic nuclei; Hy = hypothalamus. (**H**) Transgene expression detected by the alB probe. These positive regions coincide with regions identified in C and overlap the background expression of the endogenous gene.